Richard D Thompson

List of Publications by Year
in descending order

76	4,116	94433	114465
papers	citations	37 h-index	63 g-index

78	78	78	4021
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Proteomics of Medicago truncatula Seed Development Establishes the Time Frame of Diverse Metabolic Processes Related to Reserve Accumulation. Plant Physiology, 2003, 133, 664-682.	4.8	241
2	The role of the DNA-binding One Zinc Finger (DOF) transcription factor family in plants. Plant Science, 2013, 209, 32-45.	3.6	241
3	A Combined Proteome and Transcriptome Analysis of Developing Medicago truncatula Seeds. Molecular and Cellular Proteomics, 2007, 6, 2165-2179.	3.8	237
4	Analysis of HMW glutenin subunits encoded by chromosome 1A of bread wheat (Triticum aestivum L.) indicates quantitative effects on grain quality. Theoretical and Applied Genetics, 1992, 83, 373-378.	3.6	225
5	UTILLdb, a Pisum sativum in silico forward and reverse genetics tool. Genome Biology, 2008, 9, R43.	9.6	157
6	The role of the testa during development and in establishment of dormancy of the legume seed. Frontiers in Plant Science, 2014, 5, 351.	3.6	154
7	The characterization of cDNA clones coding for wheat storage proteins. Nucleic Acids Research, 1983, 11, 2961-2977.	14.5	147
8	Development and functions of seed transfer cells. Plant Science, 2001, 160, 775-783.	3.6	141
9	Transcriptional Regulation of Storage Protein Synthesis During Dicotyledon Seed Filling. Plant and Cell Physiology, 2008, 49, 1263-1271.	3.1	131
10	Establishment of Cereal Endosperm Expression Domains. Plant Cell, 2002, 14, 599-610.	6.6	116
11	Molecular characterization of BET1, a gene expressed in the endosperm transfer cells of maize.. Plant Cell, 1995, 7, 747-757.	6.6	108
12	Optimizing TILLING populations for reverse genetics in Medicago truncatula. Plant Biotechnology Journal, 2009, 7, 430-441.	8.3	106
13	Gene expression profiling of M. truncatula transcription factors identifies putative regulators of grain legume seed filling. Plant Molecular Biology, 2008, 67, 567-580.	3.9	85
14	Maize endosperm secretes a novel antifungal protein into adjacent maternal tissue. Plant Journal, 2001, 25, 687-698.	5.7	82
15	The S locus of flowering plants: when self-rejection is self-interest. Trends in Genetics, 1992, 8, 381-387.	6.7	74
16	Reserve accumulation in legume seeds. Comptes Rendus - Biologies, 2008, 331, 755-762.	0.2	72
17	Evidence for factors regulating transfer cell-specific expression in maize endosperm. Plant Molecular Biology, 1999, 41, 403-414.	3.9	70
18	Changes in gene expression in maize kernel in response to water and salt stress. Plant Cell Reports, 2006, 25, 71-79.	5.6	69

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19	Biosynthesis of the Halogenated Auxin, 4-Chloroindole-3-Acetic Acid Â Â. Plant Physiology, 2012, 159, 1055-1063.	4.8	69
20	rgf1, a mutation reducing grain filling in maize through effects on basal endosperm and pedicel development+. Plant Journal, 2000, 23, 29-42.	5.7	68
21	Model legumes contribute to faba bean breeding. Field Crops Research, 2010, 115, 253-269.	5.1	64
22	The Seed Composition of Arabidopsis Mutants for the Group 3 Sulfate Transporters Indicates a Role in Sulfate Translocation within Developing Seeds. Plant Physiology, 2010, 154, 913-926.	4.8	61
23	Exploring the nuclear proteome of Medicago truncatula at the switch towards seed filling. Plant Journal, 2008, 56, 398-410.	5.7	60
24	The S locus of flowering plants: when self-rejection is self-interest. Trends in Genetics, 1992, 8, 381-387.	6.7	57
25	Identification of a Promoter Sequence from the BETL1Gene Cluster Able to Confer Transfer-Cell-Specific Expression in Transgenic Maize. Plant Physiology, 1999, 121, 1143-1152.	4.8	55
26	The transcriptional activatorOpaque-2 controls the expression of a cytosolic form of pyruvate orthophosphate dikinase-1 in maize endosperms. Molecular Genetics and Genomics, 1996, 250, 647-654.	2.4	54
27	Evidence that auxin is required for normal seed size and starch synthesis in pea. New Phytologist, 2017, 216, 193-204.	7.3	54
28	The most abundant soluble basic protein of the stylar transmitting tract in potato (Solanum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 T	3.2	50
29	PUB1 Interacts with the Receptor Kinase DMI2 and Negatively Regulates Rhizobial and Arbuscular Mycorrhizal Symbioses through Its Ubiquitination Activity in Medicago truncatula. Plant Physiology, 2016, 170, 2312-2324.	4.8	49
30	ZEMa, a member of a novel group of MADS box genes, is alternatively spliced in maize endosperm. Nucleic Acids Research, 1995, 23, 2168-2177.	14.5	47
31	A role for an endospermâ€localized subtilase in the control of seed size in legumes. New Phytologist, 2012, 196, 738-751.	7.3	44
32	Investigation of a self-compatible mutation in Solanum tuberosum clones inhibiting S-allele activity in pollen differentially. Molecular Genetics and Genomics, 1991, 226-226, 283-288.	2.4	43
33	Alteration of GCN5 levels in maize reveals dynamic responses to manipulating histone acetylation. Plant Journal, 2003, 33, 455-469.	5.7	42
34	Interaction of maize Opaque-2 and the transcriptional co-activators GCN5 and ADA2, in the modulation of transcriptional activity. Plant Molecular Biology, 2004, 55, 239-252.	3.9	42
35	Differences in cell type-specific expression of the gene Opaque 2 in maize and transgenic tobacco. Molecular Genetics and Genomics, 1994, 244, 391-400.	2.4	40
36	Functional expression of the transcriptional activator Opaque-2 of Zea mays in transformed yeast. Molecular Genetics and Genomics, 1993, 241-241, 319-326.	2.4	38

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37	Genomeâ€wide association studies with proteomics data reveal genes important for synthesis, transport and packaging of globulins in legume seeds. New Phytologist, 2017, 214, 1597-1613.	7.3	38
38	A maize FK506-sensitive immunophilin, mzFKBP-66, is a peptidylproline cis - trans -isomerase that interacts with calmodulin and a 36-kDa cytoplasmic protein. Planta, 1998, 205, 121-131.	3.2	37
39	Sultr4;1 mutant seeds of Arabidopsis have an enhanced sulphate content and modified proteome suggesting metabolic adaptations to altered sulphate compartmentalization. BMC Plant Biology, 2010, 10, 78.	3.6	37
40	Post-Genomics Studies of Developmental Processes in Legume Seeds. Plant Physiology, 2009, 151, 1023-1029.	4.8	36
41	Genetic and genomic analysis of legume flowers and seeds. Current Opinion in Plant Biology, 2006, 9, 133-141.	7.1	35
42	The b-32 protein from maize endosperm: characterization of genomic sequences encoding two alternative central domains. Plant Molecular Biology, 1990, 14, 1031-1040.	3.9	34
43	Translation of the mRNA of the Maize Transcriptional Activator Opaque-2 Is Inhibited by Upstream Open Reading Frames Present in the Leader Sequence. Plant Cell, 1993, 5, 65.	6.6	34
44	Regulation of Storage Protein Synthesis in Cereal Seeds: Developmental and Nutritional Aspects. Journal of Plant Physiology, 1995, 145, 606-613.	3.5	32
45	Regulation of cytosolic pyruvate, orthophosphate dikinase expression in developing maize endosperm. Plant Molecular Biology, 1996, 31, 45-55.	3.9	32
46	In vitro culture of immature M. truncatula grains under conditions permitting embryo development comparable to that observed in vivo. Plant Science, 2006, 170, 1052-1058.	3.6	32
47	DASH transcription factor impacts Medicago truncatula seed size by its action on embryo morphogenesis and auxin homeostasis. Plant Journal, 2015, 81, 453-466.	5.7	31
48	Nitrogen and hormonal responsiveness of the 22 kDa alpha-zein and b-32 genes in maize endosperm is displayed in the absence of the transcriptional regulator Opaque-2. Plant Journal, 1997, 12, 281-291.	5.7	29
49	Structural and functional analysis of an Opaque-2-related gene from sorghum. Plant Molecular Biology, 1994, 24, 515-523.	3.9	28
50	Role of a receptor-like kinase K1 in pea Rhizobium symbiosis development. Planta, 2018, 248, 1101-1120.	3.2	25
51	Molecular analysis of theBg-rbg transposable element system ofZea mays L.. Molecular Genetics and Genomics, 1991, 227, 91-96.	2.4	23
52	Molecular analysis of opaque-2 alleles from Zea mays L. reveals the nature of mutational events and the presence of a hypervariable region in the 5â€² part of the gene. Genetical Research, 1995, 65, 11-19.	0.9	20
53	The activation domain of the maize transcription factor Opaque-2 resides in a single acidic region. Nucleic Acids Research, 1997, 25, 756-763.	14.5	19
54	Subcellular localisation of BETL-1, -2 and -4 in Zea mays L. endosperm. Sexual Plant Reproduction, 2002, 15, 85-98.	2.2	19

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55	A Cytokinin Signaling Type-B Response Regulator Transcription Factor Acting in Early Nodulation. Plant Physiology, 2020, 183, 1319-1330.	4.8	19
56	The accumulation of zein polypeptides and zein mRNA in cultured endosperms of maize is modulated by nitrogen supply. Plant Journal, 1993, 3, 325-334.	5.7	17
57	Anatomical bases of sexâ€•and sizeâ€•related acoustic variation in herring gull alarm calls. Journal of Avian Biology, 2014, 45, 157-166.	1.2	17
58	In situ expression of two storage protein genes in relation to histo-differentiation at mid-embryogenesis in Medicago truncatula and Pisum sativum seeds. Journal of Experimental Botany, 2005, 56, 2019-2028.	4.8	16
59	In vitro auxin treatment promotes cell division and delays endoreduplication in developing seeds of the model legume species Medicago truncatula. Physiologia Plantarum, 2013, 148, 549-559.	5.2	16
60	Î²-Amyrin Synthase1 Controls the Accumulation of the Major Saponins Present in Pea (Pisum) Tj ETQq0 0 0 rgBT /Overlock 10	3.1	16
61	Post-phloem protein trafficking in the maize caryopsis: zmTRXh1, a thioredoxin specifically expressed in the pedicel parenchyma of Zea mays L., is found predominantly in the placentochalaza. Plant Molecular Biology, 2002, 50, 743-756.	3.9	14
62	Structural Variations in LysM Domains of LysM-RLK PsK1 May Result in a Different Effect on Peaâ€“Rhizobial Symbiosis Development. International Journal of Molecular Sciences, 2019, 20, 1624.	4.1	12
63	Genetic Regulation of Carbohydrate and Protein Accumulation in Seeds. Advances in Cellular and Molecular Biology of Plants, 1997, , 479-522.	0.2	11
64	The seed nuclear proteome. Frontiers in Plant Science, 2012, 3, 289.	3.6	9
65	Genetic manipulations of protein quality in maize grain. Field Crops Research, 1996, 45, 37-48.	5.1	7
66	Turning fields into grains. Nature, 2000, 408, 39-41.	27.8	6
67	Genetic Control of Endosperm Development. , 1999, , 185-197.		4
68	PeaMUST (Pea MultiStress Tolerance), a multidisciplinary French project uniting researchers, plant breeders, and the food industry. , 2021, 3, e108.		4
69	The role of multiple binding sites in the activation of zein gene expression by. Molecular Genetics and Genomics, 1996, 252, 723.	2.4	4
70	A Novel Recombinant of Phage Lambda and a Conserved 3000-Base-Pair Fragment of Xenopus laevis Ribosomal Deoxyribonucleic Acid Produced by Restriction with Endonucleases Hind III/BamI. Biochemical Society Transactions, 1978, 6, 1232-1233.	3.4	2
71	Functional Genomics and Seed Development in Medicago truncatula: An Overview. Methods in Molecular Biology, 2018, 1822, 175-195.	0.9	2
72	Targeting Induced Local Lesions IN Genomes (TILLING) in Medicago truncatula. Methods in Molecular Biology, 2018, 1822, 71-82.	0.9	2

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73	The Tobacco BY-2 Cell Line as a Model System to Understand in Planta Nuclear Coactivator Interactions. Biotechnology in Agriculture and Forestry, 2004, , 316-331.	0.2	2
74	Networks of Seed Storage Protein Regulation in Cereals and Legumes at the Dawn of the Omics Era. , 2012, , 187-210.		1
75	Metabolic Specialization of Maternal and Filial Tissues. , 2012, , 407-432.		0
76	Genetic and Molecular Studies on Endosperm Storage Proteins in Maize. , 1991, , 627-634.		0